

L. Helms

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/293,533

DATE: 10/19/2000
TIME: 21:36:24

INPUT SET: S36024.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#9

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Chatterjee, Malaya
6 Foon, Kenneth A.
7 Chatterjee, Sunil K.
8
9 (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
10 TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
11
12 (iii) NUMBER OF SEQUENCES: 66
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: MORRISON & FOERSTER
16 (B) STREET: 755 PAGE MILL ROAD
17 (C) CITY: PALO ALTO
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 94304-1018
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: 09/293,533
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US/08/752,844
35 (B) FILING DATE:
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Schiff, J. Michael
39 (B) REGISTRATION NUMBER: 40,253
40 (C) REFERENCE/DOCKET NUMBER: 30414-20002.21
41
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: (415) 813-5600
44 (B) TELEFAX: (415) 494-0792
45 (C) TELEX: 706141
46

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47
48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 447 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: DNA (genomic)
57
58
59 (ix) FEATURE:
60 (A) NAME/KEY: CDS
61 (B) LOCATION: 1..447
62
63 (ix) FEATURE:
64 (A) NAME/KEY: mat_peptide
65 (B) LOCATION: 58
66
67
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70 ATG AAG TTG CCT GTT AGG CTG TTG GTG CTG ATG TTC TGG ATT CCT GCT 48
71 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
72 -19 -15 -10 -5
73
74 TCC AGC GAT GAT GTT TTC ATG ACC CAA ACT CCA CTC TCC CTG CCT GTC 96
75 Ser Ser Asp Asp Val Phe Met Thr Gln Thr Pro Leu Ser Leu Pro Val
76 1 5 10
77
78 AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC ATT 144
79 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
80 15 20 25
81
82 GTA CAT AGT AAT GGA AAC ACC TAT TTA GAA TGG TAC CTA CAG AAA CCA 192
83 Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
84 30 35 40 45
85
86 GGC CAG TCT CCA AAC CTC CTG ATC TAC TTT GTT TCC AAC CGA TTT TCT 240
87 Gly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val Ser Asn Arg Phe Ser
88 50 55 60
89
90 GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCA GGG ACA GAT TTC ACA 288
91 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
92 65 70 75
93
94 CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TAC TGC 336
95 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
96 80 85 90
97
98 TTT CAA GGT TCA CAT GTT CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG 384
99 Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu

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100          95          100          105
101
102 GAA ATC AAA CGG GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA      432
103 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
104 110          115          120          125
105
106 TCC AGT AAG CTT GGG      447
107 Ser Ser Lys Leu Gly
108          130
109
110
111 (2) INFORMATION FOR SEQ ID NO:2:
112
113 (i) SEQUENCE CHARACTERISTICS:
114 (A) LENGTH: 149 amino acids
115 (B) TYPE: amino acid
116 (D) TOPOLOGY: linear
117
118 (ii) MOLECULE TYPE: protein
119
120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
121
122 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
123 -19          -15          -10          -5
124
125 Ser Ser Asp Asp Val Phe Met Thr Gln Thr Pro Leu Ser Leu Pro Val
126          1          5          10
127
128 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
129 15          20          25
130
131 Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
132 30          35          40          45
133
134 Gly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val Ser Asn Arg Phe Ser
135          50          55          60
136
137 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
138          65          70          75
139
140 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
141          80          85          90
142
143 Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
144 95          100          105
145
146 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
147 110          115          120          125
148
149 Ser Ser Lys Leu Gly
150          130
151
152 (2) INFORMATION FOR SEQ ID NO:3:

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153
154      (i) SEQUENCE CHARACTERISTICS:
155          (A) LENGTH: 458 base pairs
156          (B) TYPE: nucleic acid
157          (C) STRANDEDNESS: single
158          (D) TOPOLOGY: linear
159
160      (ii) MOLECULE TYPE: DNA (genomic)
161
162
163      (ix) FEATURE:
164          (A) NAME/KEY: CDS
165          (B) LOCATION: 1..456
166
167      (ix) FEATURE:
168          (A) NAME/KEY: mat_peptide
169          (B) LOCATION: 58
170
171
172      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
173
174      ATG GCT GTC TTG GGG CTG CTC TTC TGC CTG GTG ACA TTC CCA AGC TGT      48
175      Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
176      -19          -15          -10          -5
177
178      GTC CTG TCC CAG GTG CAG GTG AAG GAG TCA GGA CCT TTC CTG GTG CCC      96
179      Val Leu Ser Gln Val Gln Val Lys Glu Ser Gly Pro Phe Leu Val Pro
180          1          5          10
181
182      CCC TCA CAG AGC CTG TCC ATC ACA TGC ACT GTC TCA GGG TTC TCA TTA      144
183      Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
184          15          20          25
185
186      ACC ACC TAT GGT GTA AGC TGG ATT CGC CAG CCT CCA GGA AAG GGT CTG      192
187      Thr Thr Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
188          30          35          40          45
189
190      GAG TGG CTG GGA GCA ATT TGG GGT GAC GGG ACC ACA AAT TAT CAT TCA      240
191      Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser
192          50          55          60
193
194      GCT CTC ATA TCC AGA CTG AGC ATC AGC AAG GAT AAC TCC AAG AGC CAA      288
195      Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln
196          65          70          75
197
198      GTT TTC TTA AAA CTG AAC AGT CTG CAA ACT GAT GAC ACG GCC ACG TAC      336
199      Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr
200          80          85          90
201
202      TAC TGT GCC AAA CTG GGT AAC TAC GAT GCT CTG GAC TAC TGG GGT CAA      384
203      Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp Tyr Trp Gly Gln
204          95          100          105
205

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206 GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC GTC 432
207 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro Val
208 110 115 120 125

209
210 TAT CCA TTG GTC CCT GGA AGC TTG GG 458
211 Tyr Pro Leu Val Pro Gly Ser Leu
212 130
213
214

215 (2) INFORMATION FOR SEQ ID NO:4:

216
217 (i) SEQUENCE CHARACTERISTICS:

218 (A) LENGTH: 152 amino acids

219 (B) TYPE: amino acid

220 (D) TOPOLOGY: linear

221
222 (ii) MOLECULE TYPE: protein
223

224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

225
226 Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
227 -19 -15 -10 -5
228

229 Val Leu Ser Gln Val Gln Val Lys Glu Ser Gly Pro Phe Leu Val Pro
230 1 5 10
231

232 Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
233 15 20 25
234

235 Thr Thr Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
236 30 35 40 45
237

238 Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser
239 50 55 60
240

241 Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln
242 65 70 75
243

244 Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr
245 80 85 90
246

247 Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp Tyr Trp Gly Gln
248 95 100 105
249

250 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro Val
251 110 115 120 125
252

253 Tyr Pro Leu Val Pro Gly Ser Leu
254 130
255

256 (2) INFORMATION FOR SEQ ID NO:5:

257
258 (i) SEQUENCE CHARACTERISTICS:

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SEQUENCE VERIFICATION REPORT
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